

Admixture-aware scan for signatures of local adaptation

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 An abbreviated version of this protocol was published in eLIFE in Sep 2021

Local adaptation and archaic introgression shape global diversity at human structural variant loci

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Detailed protocol

Dear Yechao,

Thank you very much for your interest in our work. The requested information about the 220 frequency-differentiated SVs can be found in the Zenodo repository associated with the paper at <https://doi.org/10.5281/zenodo.4469975>. We noticed that the relevant file ([selscan_res.txt.gz](#)) we had previously posted was truncated and only included data from a single ancestry component. We have updated the file to include the complete set of results, available for direct download at https://zenodo.org/record/6245629/files/selscan_res.txt.gz?download=1.

The 220 frequency-differentiated SVs can be extracted from this table by selecting all rows for which the percentile ("snp_perc" column) is greater than 0.999. A total of 226 rows meet this criterion, of which 220 SV IDs are unique (as a few SVs are outliers in multiple ancestry components).

Thanks again, and please let us know if you have any other questions.

Best,

Rajiv McCoy and Stephanie Yan

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Yan, S. and McCoy, R. C.(2022). Admixture-aware scan for signatures of local adaptation. Bio-protocol Preprint. bio-protocol.org/prep1543.
2. Yan, S. M., Sherman, R. M., Taylor, D. J., Nair, D. R., Bortvin, A. N., Schatz, M. C. and McCoy, R. C.(2021). Local adaptation and archaic introgression shape global diversity at human structural variant loci. eLIFE. DOI: [10.7554/eLife.67615](https://doi.org/10.7554/eLife.67615)

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